



SEQUENCE LISTING

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<120> NOVEL SERINE PROTEASE BSSP5

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<140> 09/856,319

<141> 2001-05-21

<150> JP 10/347806

<151> 1998-11-20

<150> PCT JP99/06473

<151> 1999-11-19

<160> 32

<170> PatentIn version 3.1

<210> 1

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ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc 97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
-20 -15 -10 -5

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Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
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ccc tgg cag gtg tcc ctg cag gac agc agc ggc ttc cac ttc tgc ggt 193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly
15 20 25

ggt tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat 241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
30 35 40

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gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca      289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
45                               50                               55                               60

tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca      337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr
                               65                               70                               75

cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg      385
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu
                               80                               85                               90

aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc      433
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys
95                               100                               105

ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc      481
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr
110                               115                               120

acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cat      529
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His
125                               130                               135                               140

ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag      577
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln
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tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt ggc gca      625
Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala
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ggt gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag      673
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln
                               175                               180                               185

aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa      721
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys
190                               195                               200

aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc      769
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe
205                               210                               215                               220

agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc      822
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
                               225                               230

cccagctcaa cccatttaaa ggacccaggc cctgtcccat catgcattca tgtctgtctt      882

cctggctcag gagaaagaag aggctgttga ggggtccgact ccctacttgg acttctggca      942

cagaaggggc tgagtgactc cttgagtagc agtggtcttt cctagagtag ccatgccgtg      1002

gccggggccc ccacccctcc tccagggcaa ccccttggtc ctacagcaag aagccagaac      1062

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Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
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Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu
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Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
 35 40 45

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
 50 55 60

Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
 65 70 75

Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
 80 85 90 95

Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
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Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
 115 120 125

Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His Leu Gln Gln
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Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Asp
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Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
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 Ile Thr Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn
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 Ala Val Pro Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr
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 ggc ttc cac ttc tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc 245
 Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val
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 acg gct gcc cac tgc caa gtc acg cct gga cgc cac ttt gtc gtt ttg 293
 Thr Ala Ala His Cys Gln Val Thr Pro Gly Arg His Phe Val Val Leu
 40 45 50
 gga gaa tat gac cga tct tcc aat gct gaa cct gtg cag gtc ctc tcg 341
 Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Val Gln Val Leu Ser
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 Ile Ala Arg Ala Ile Thr His Pro Asn Trp Asn Ala Asn Thr Met Asn
 75 80 85
 aat gac ctg act ctc ctg aag ctt gcc tcg cca gcc cgg tac aca gca 437
 Asn Asp Leu Thr Leu Leu Lys Leu Ala Ser Pro Ala Arg Tyr Thr Ala
 90 95 100

caa gtc tca cca gtc tgc ctg gct tcc aca aac gag gca ctg cct tcg 485
 Gln Val Ser Pro Val Cys Leu Ala Ser Thr Asn Glu Ala Leu Pro Ser
 105 110 115
 ggg ctc acc tgt gtc acc act ggc tgg ggc cga atc agt ggt gtg ggc 533
 Gly Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Ile Ser Gly Val Gly
 120 125 130
 aat gtg aca cca gct cgc ctg cag caa gtt gtt cta ccc ctg gtc act 581
 Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val Leu Pro Leu Val Thr
 135 140 145 150
 gtg aat cag tgt cgg cag tac tgg ggt gca cgc att acc gat gcc atg 629
 Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile Thr Asp Ala Met
 155 160 165
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 Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly
 170 175 180
 ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att ggg att 725
 Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile
 185 190 195
 gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg tac 773
 Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met Tyr
 200 205 210
 act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac 821
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-15 -10 -5

Arg Ile Val Asn Gly Glu Asn Ala Val Pro Gly Ser Trp Pro Trp Gln
-1 1 5 10 15

Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe Cys Gly Gly Ser Leu
20 25 30

Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys Gln Val Thr Pro
35 40 45

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
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Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His Pro Asn
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Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu Ala
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Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
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Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp
115 120 125

Gly Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
130 135 140

Val Val Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
145 150 155

Ala Arg Ile Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser
160 165 170 175

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
180 185 190

Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
195 200 205

Ile Gln Ala Pro Ala Met Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
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Ile Asn Gln Val Met Ala Tyr Asn
225 230

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tgctgcccc tttgacgacg atgacaagga tccgaattc 99

<210> 6
 <211> 99
 <212> DNA
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<220>
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 aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

<210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence.

<400> 7
 ttggtgcatg gcgga 15

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence.

<400> 8
 tcctcgagac ttggcctgaa tggtttt 27

<210> 9
 <211> 35
 <212> DNA
 <213> Artificial Sequence

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 <223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin.

<400> 9
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<210> 10
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin.

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 tgaagcttgc catggaccaa cttgtcatc 29

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p TrypHis.

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<210> 12
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p TrypSigTag.

<400> 12
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<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p FBTrypSigTag.

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 caaatgtggt atggctg 17

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 <211> 20
 <212> DNA
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 <223> n is a, c, g or t.

<220>
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 <222> (12)..(12)
 <223> n is a, c, g or t.

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<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify conserved region of se
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<223> n is a, c, g or t.

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<221> misc_feature
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<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSP5 (forward).

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<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSP5 (forward).

<400> 17
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<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSP5 (reverse).

<400> 18

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20

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse).

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 gaatcagtgc cggcagtact 20

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5F1 to amplify full length hBSSP5 (forward).

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<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5F2 to amplify mature hBSSP5-encoding region (forward).

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<210> 22
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP5R1/E to amplify full length hBSSP5 (reverse).

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<210> 23
 <211> 18
 <212> DNA
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<220>
 <223> Designed oligonucleotide primer designated as hBSSP5R4 for RT-PCR (reverse).

<400> 23
cctggcacga ggaggcac 18

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE f
or mBSSP5 (forward).

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<210> 25
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE f
or mBSSP5 (forward)

<400> 25
gaatcagtgt cggcagt 17

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify
full length mBSSP5 (forward).

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<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5F mature to a
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<400> 27
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<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5R2 for RACE f

or mBSSP5 (reverse).

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<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<210> 30
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<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP5R3/E to amplify full length mBSSP5 (reverse).

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gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117